TETTRIs

Funded by
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POLICY BRIEF

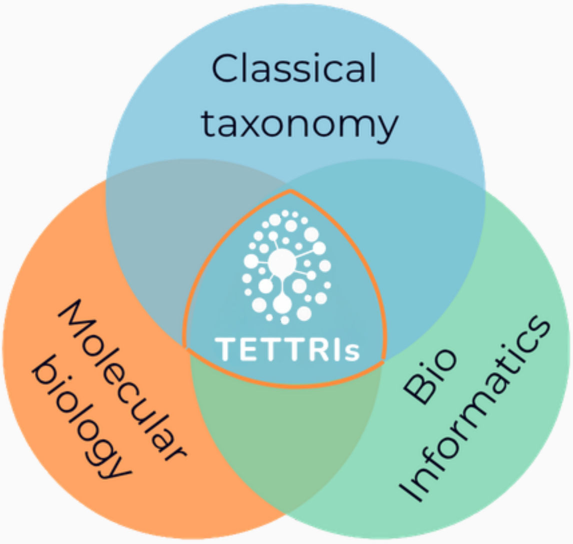
Scaling Biodiversity Assessment through Integrating Innovative Molecular Tools and Workflows in Taxonomy

Executive summary

The global biodiversity crisis requires rapid and accurate creation of an inventory of life on Earth. Traditional taxonomy, while foundational, faces a "bottleneck" due to the sheer volume of species and the complexity of cryptic species complexes. The **TETTRIs** project is addressing this by developing and implementing state-of-the-art molecular tools—ranging from single-locus DNA barcoding to screening entire genomes —that bridge the gap between high-throughput monitoring and expert-led taxonomic description.

Modernizing the Taxonomic Workflow: A Marriage of Disciplines

Traditional taxonomy has evolved into a "marriage" between classical morphology, phylogenetics, molecular biology, and bioinformatics, a synergy known as **integrative taxonomy**. Far from being a static field, it is characterized by fast-developing innovations, such as the recent implementation of Oxford Nanopore Technologies or third generation sequencing, which offers portable, cost-effective, and rapid data generation.



The **TETTRIs** project directly contributes to this evolution by advancing the tools and skills necessary for modern integrative workflows:

- **Democratizing complex analysis**: TETTRIs lowers the barrier for researchers who may have limited bioinformatic skills by providing intuitive platforms like SPART EXPLORER. This user-friendly web platform allows taxonomists to perform single-locus species delimitation and comparative visualizations.
- **Open Science and FAIR sharing:** To improve the robust detection and delimitation of biodiversity, including cases of potential cryptic diversity (groups that are morphologically very similar or indistinguishable but genetically distinct), TETTRIs promotes the development and open-source sharing of innovative pipelines, such as Amplipiper. These resources ensure that advanced molecular methodologies are FAIR (Findable, Accessible, Interoperable, and Reusable) for the entire scientific community.
- **Capacity building and knowledge transfer**: Beyond tool development, TETTRIs emphasizes training a new generation of taxonomists. This is achieved through capacity building and knowledge transfer via associated third-party projects like CRYPTERS and NEXTRAD, which demonstrate how these molecular tools can be applied to increase biodiversity knowledge in global biodiversity hotspots.

Bridging the Gap: Accessible Tools for Species Discovery

A core challenge in modern taxonomy is the "bioinformatics hurdle." TETTRIs has developed a strategy to ensure that state-of-the-art molecular methods are available to all researchers, functioning as two halves of a single, powerful conversation between data and expertise.

I. THE MOLECULAR/BIOINFORMATICS PARTNER: AMPLIPIPER

The focus:
Automated data processing and high-resolution genetic reconstruction.

The innovation:
An open-source pipeline designed to process multi-locus data, specifically optimized for cost-effective Oxford Nanopore Technologies sequencing.

The role:
AmpliPiper does the "heavy lifting" by taking raw, complex sequencing reads and performing haplotype-specific reconstruction. This allows the tool to "untangle" genetic sequences even in difficult cases like polyploid organisms or mixed samples. By automating the journey from the lab bench to a clean phylogenetic tree, it provides the robust genetic evidence needed for modern species discovery and delimitation.

II. THE INTEGRATIVE/EXPERT PARTNER: SPART EXPLORER

The focus:
Human-led interpretation and comparative visualization.

The innovation:
A user-friendly web platform that allows taxonomists to infer and compare species "partitions" (grouping hypotheses) without writing a single line of code.

The role:
SPART EXPLORER is where the genetic data meets biological reality. It takes the outputs (like those from AmpliPiper) and provides an interface for the Integrative/Expert partner. Here, a taxonomist can overlay molecular clusters with morphological traits or distributional data. This comparative visualization allows the researcher to see where different lines of evidence align, facilitating a final, expert-led taxonomic decision.

Building Capacity and European Connectivity

Innovation is only effective if it is shared. TETTRIs emphasizes Open Science and knowledge transfer.

FAIR DATA & OPEN SOURCE:

By making innovative pipelines open-source via GitHub, ensuring methods are Findable, Accessible, Interoperable, and Reusable (FAIR) and providing solutions for access to computing resources.

THE IMPORTANCE OF VOUCHERS:

A critical standard promoted by TETTRIs is the linking of DNA sequences to reference voucher specimens in Natural History Collections using persistent identifiers. These collection institutions provide the essential service of hosting the physical evidence behind the digital sequence, ensuring scientific reproducibility.

KNOWLEDGE TRANSFER:

Associated projects like CRYPTERS and NEXTRAD act as proof-of-concepts, demonstrating how these tools build capacity in biodiversity hotspots and foster transboundary collaboration between resource-rich and biodiversity-rich regions.

STRATEGIC CONNECTIONS:

By aligning with networks like iBOL Europe, ERGA, BGE and DiSSCo, and integrating workflows into the EU Galaxy Platform, TETTRIs ensures its tools are embedded within the wider European biodiversity research landscape.

SPOTLIGHT ON IMPACT:
UNCOVERING HIDDEN DIVERSITY WITH CRYPTERS

This project illustrates the urgent need for molecular tools in biodiversity conservation. Focusing on the endangered Alpine wolf spider (Vesubia jugorum), the project uses advanced multilocus markers and SNPs (Single Nucleotide Polymorphisms) to detect "cryptic diversity"— biological species that are invisible using traditional taxonomic approaches.

- **The goal:** By identifying isolated populations that may be evolving separately due to the extreme Alpine environment, CRYPTERS provides the data needed for Species Distribution Models.

- **The policy link:** These genetic insights allow red list assessors and park managers to move beyond general protections and create targeted conservation plans that account for the small-scale endemism of these species and how they will respond to climate change.

Image: Vesubia jugorum. Courtesy of CRYPTERS

Strategic Recommendations for Policymakers

1 ESTABLISH "MUSEUM HUBS"

Support Natural History Museums as central innovation hubs. Museums should provide the infrastructure for molecular tool access and training for taxonomists, while also ensuring the long-term preservation of voucher specimens (physical evidence), including type specimens, and developing innovative tools to enhance the digital accessibility of natural history collections.

2 MANDATE LINKED DATA

All biodiversity monitoring funding should require that DNA sequences are persistently linked to physical voucher specimens through globally unique persistent identifiers (PIDs) in recognized collection institutions to ensure traceability and scientific reproducibility.

3 INVEST IN TRANSBOUNDARY PARTNERSHIPS

Encourage collaborations that pair skill-rich institutions with biodiversity-rich countries to ensure global equity in the fight against extinction.

4 ADOPT ADVANCED INDICATORS

Beyond simple species counts and functional diversity metrics, policymakers should incorporate phylogenetic diversity as a standard indicator of conservation value, reflecting evolutionary potential, resilience, and diversity in ecosystem function.

CASE STUDY 1:
Resolving complex diversity with AmpliPiper

Researchers used the AmpliPiper pipeline to analyze hoverfly (Syrphidae) datasets using cost-effective Oxford Nanopore sequencing. By moving beyond single-locus barcodes to multi-locus data, the pipeline automatically reconstructed specific genetic haplotypes and generated phylogenetic trees in one automated step. This high-resolution approach was as accurate as expensive "gold-standard" methods, demonstrating that complex genomic research can now be conducted rapidly and locally by any taxonomic lab.

CASE STUDY 2:
Efficiency in species delimitation

The practical application of these strategic shifts is demonstrated by the SPART EXPLORER platform. In a case study involving Madascincus lizards, researchers simultaneously compared 16 different species hypotheses—integrating DNA and morphology—in less than a minute. This efficiency allows researchers to focus on the high-level interpretation required for conservation, rather than getting bogged down in tedious manual data processing.

Image (right):
Madascincus polleni on iNaturalist, CC-by © Lennart Hudel

CASE STUDY 3:
Solving "Island Radiations" with NEXTRAD

Traditional plant DNA barcoding often fails to distinguish species that have evolved rapidly on islands. The NEXTRAD project addresses this by applying advanced genomic tools to the Lotus genus in Macaronesia. Through the use of multiple high-throughput sequencing approaches (Angiosperms-353 and DArTseq), combined with morphological traits and habitat information, the project is uncovering hidden species and refining the taxonomy of this enigmatic plant lineage, including the identification of a species now extinct in the wild. This work creates a repeatable standard for protecting endangered flora in the world’s most biodiverse and rapidly changing island ecosystems.

Image: *Lotus maculatus* on iNaturalist, CC-by © christoph_moning

References

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training, research and innovations

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TETTRIs Grant Agreement 101081903

Duration: December 2022 - May 2026
Budget: € 5.997.636
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Bridging the Gender Gap in research by Enhancing the role of Female Taxonomists

Source: *Image from Getty Images*

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